CLAIMS

1. HIV-2 retrovirus or variance of this virus, which retrovirus has infectious properties with respect to human T4 lymphocytes and the essential morphological and immunological properties of any of the retroviruses deposited at the CNCM under n° I-502, I-532, I-642 and I-643.

2. The purified retrovirus of claim 1 which possesses the following properties :

- the preferred target for the HIV-2 retrovirus consists of human Leu 3 cells (or T4 lymphocytes) and for permanent cell lines derived of said T4 lymphocytes ;
- it is cytotoxic for the human T4 lymphocytes which it infects ;
- it has a reverse transcriptase activity which requires the presence of Mg^{2+} ions and has a strong affinity for poly adenylate oligodeoxythymidylate (poly(A)-oligo(dT) 12-18) ;
- it has a density of approximately 1.16 in a sucrose gradient ;
- it has a mean diameter of 140 nanometres and a core having mean diameter of 41 nanometres ;
- it can be cultivated in permanent cell lines expressing the T4 protein ;
- it is not infectious in T8 lymphocytes ;
- the lysates of this virus contain p26 protein which does not crossreact immunologically with p24 protein of the HTLV-1 virus or of the HTLV-2 ;
- said lysates further contain p-16 protein which is not recognized immunologically by p19 protein of HTLV-1 or of HTLV-2 in radioimmunoprecipitation assays ;
- said lysates further contain an envelope glycoprotein having a molecular weight of the order of 130,000-140,000 which does not crossreact immunologically with

gp110 of HTLV-1 retrovirus ;

- said lysates further contain a molecule which can be labelled by ^{35}S-cystein, having an apparent molecular weight of about 36,000 ;

- the genomic RNA of HIV-2 hybridizes neither with the genomic RNA, nor with the ENV gene, nor with the LTRs of HIV-1 under stringent conditions ;

- the genomic RNA of HIV-2 hybridizes weakly under non-stringent conditions with nucleotide sequences of the GAG region of the HIV-1 genome.

3. The retrovirus of claim 2 whose lysates also contain a molecule having an apparent molecular weight of 42,000-45,000

4. The retrovirus of any of claims 1 to 3, wherein the nucleotidic sequence of its genomic RNA which comprises the R region and the U3 region also comprises a nucleotidic sequence which corresponds with the following nucleotide sequence :

GTGGAAGGCGAGACTGAAAGCAAGAGGAATACCATTTAGTTAAAGGACAG
GAACAGCTATACTTGGTCAGGGCAGGAAGTAACTAACAGAAACAGCTGAG
ACTGCAGGGACTTTCCAGAAGGGGCTGTAACCAAGGGAGGGACATGGGAG
GAGCTGGTGGGGAACGCCTCATATTCTCTGTATAATATACCCGCTGCTTG
CATTGTACTTCAGTCGCTCTGCGGAGAGGCTGGCAGATTGAGCCCTGGAG
GATCTCTCCAGCACTAGACGGATGAGCCTGGGTGCCCTGCTAGACTCTCA
CCAGCACTTGGCCGGTGCTGGCAGACGGCCCCACGCTTGCCTGCTTAAAA
ACCTTCCTTAATAAAGCTGCAGTAGAAGCA

5. The retrovirus of anyone of claims 1 to 4 whose genomic RNA also contains a GAG sequence which corresponds with the following nucleotide sequence :

GAGRODD .

```
ATGGGCGCGAGAAACTCCGTCTTGAGAGGGAAAAAAGCAGATGAA
TTAGAAAGAATCAGGTTACGGCCCGGCGGAAAGAAAAAGTACAGG
CTAAAACATATTGTGTGGGCAGCGAATAAATTGGACAGATTCGGA
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TTAGCAGAGAGCCTGTTGGAGTCAAAAGAGGGTTGTCAAAAAATT
CTTACAGTTTTAGATCCAATGGTACCGACAGGTTCAGAAAATTTA
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GAAGAGAAAGTGAAAGATACTGAAGGAGCAAAACAAATAGTGCGG
                300
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ACAAGTAGACCAACAGCACCATCTAGCGAGAAGGGAGGAAATTAC
                400
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CCCCGAACCCTAAATGCCTGGGTAAAATTAGTAGAGGAAAAAAAG
TTCGGGGCAGAAGTAGTGCCAGGATTTCAGGCACTCTCAGAAGGC
  500
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CATCAAGCAGCCATGCAGATAATCAGGGAGATTATCAATGAGGAA
                600
GCAGCAGAATGGGATGTGCAACATCCAATACCAGGCCCCTTACCA
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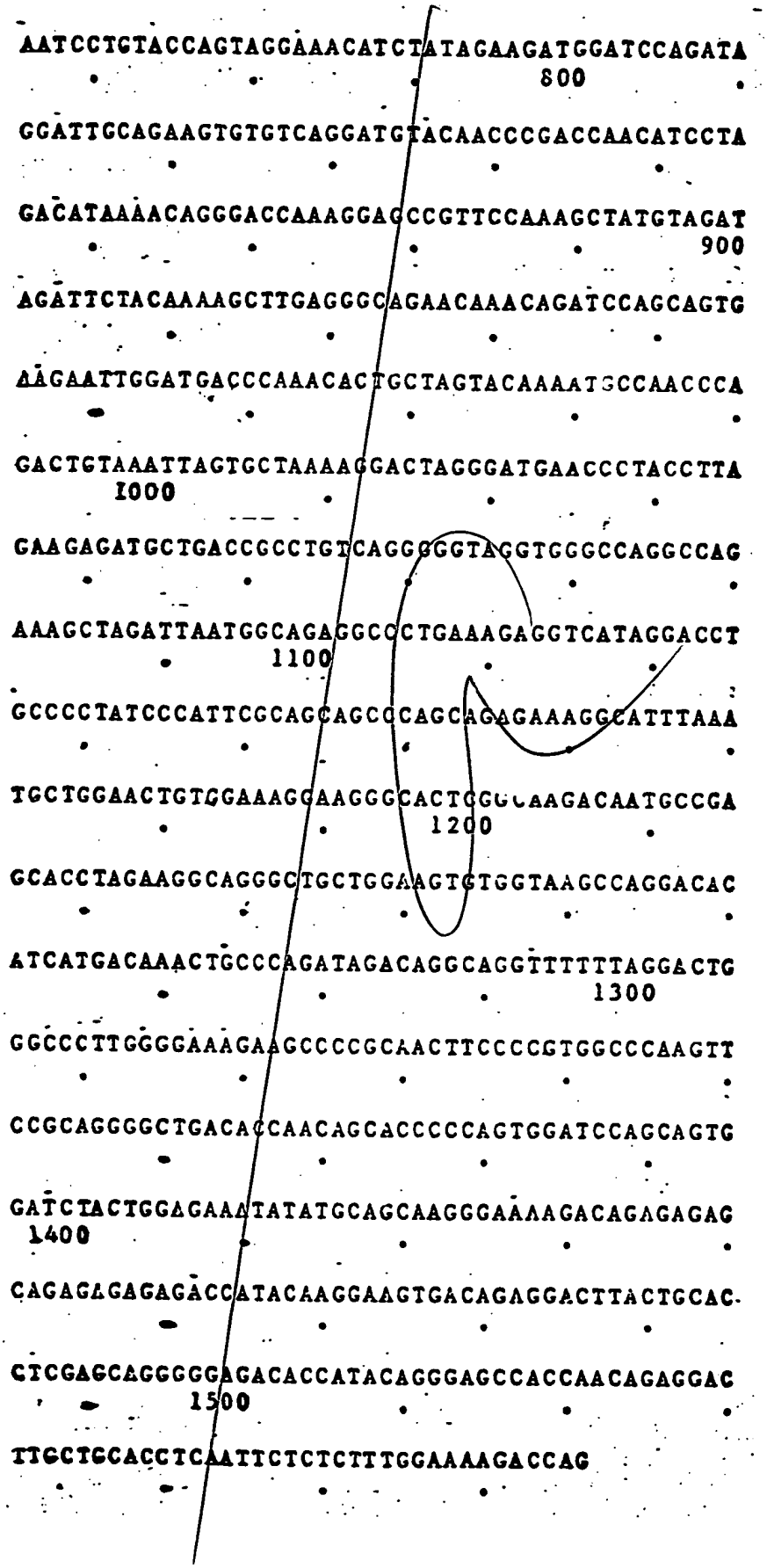
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GACTGTAAATTAGTGCTAAAAGGACTAGGGATGAACCCTACCTTA
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1400
CAGAGAGAGAGACCATACAAGGAAGTGACAGAGGACTTACTGCAC
CTCGAGCAGGGGGAGACACCATACAGGGAGCCACCAACAGAGGAC
1500
TTGCTGCACCTCAATTCTCTCTTTGGAAAAGACCAG

6. The retrovirus of anyone of claims 1 to 5 whose genomic RNA contains an ENV sequence which corresponds with the following nucleotide sequence :

ENVRN

```
ATGATGAATCAGCTGCTTATTGCCATTTTATTAGCTAGTGCTTGC

TTAGTATATTGCACCCAATATGTAACTGTTTTCTATGGCGTACCC

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                100

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  500

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                600

ACAGAATCATGTGACAAGCACTATTGGGATGCTATAAGGTTTAGA

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                          700

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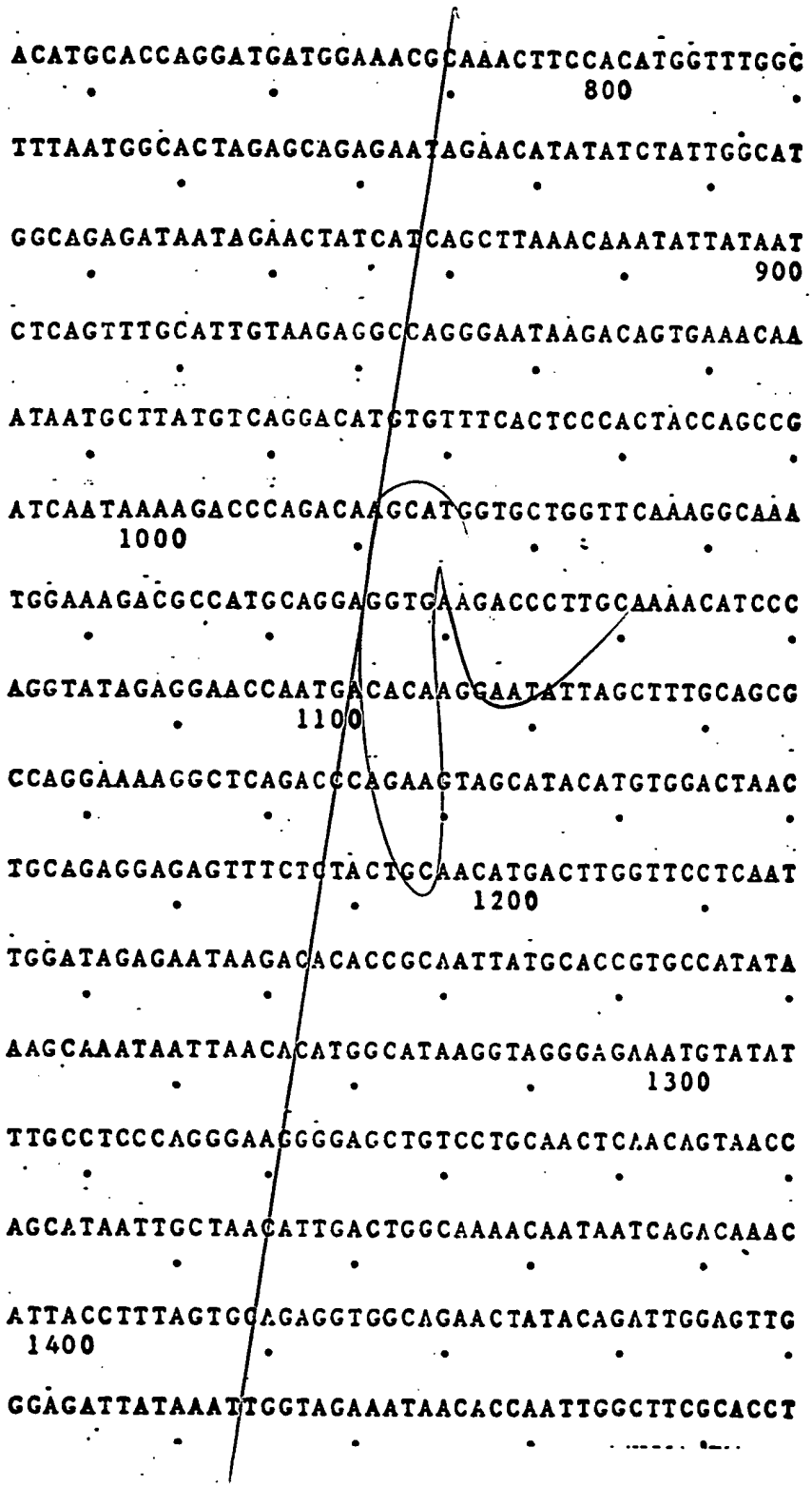
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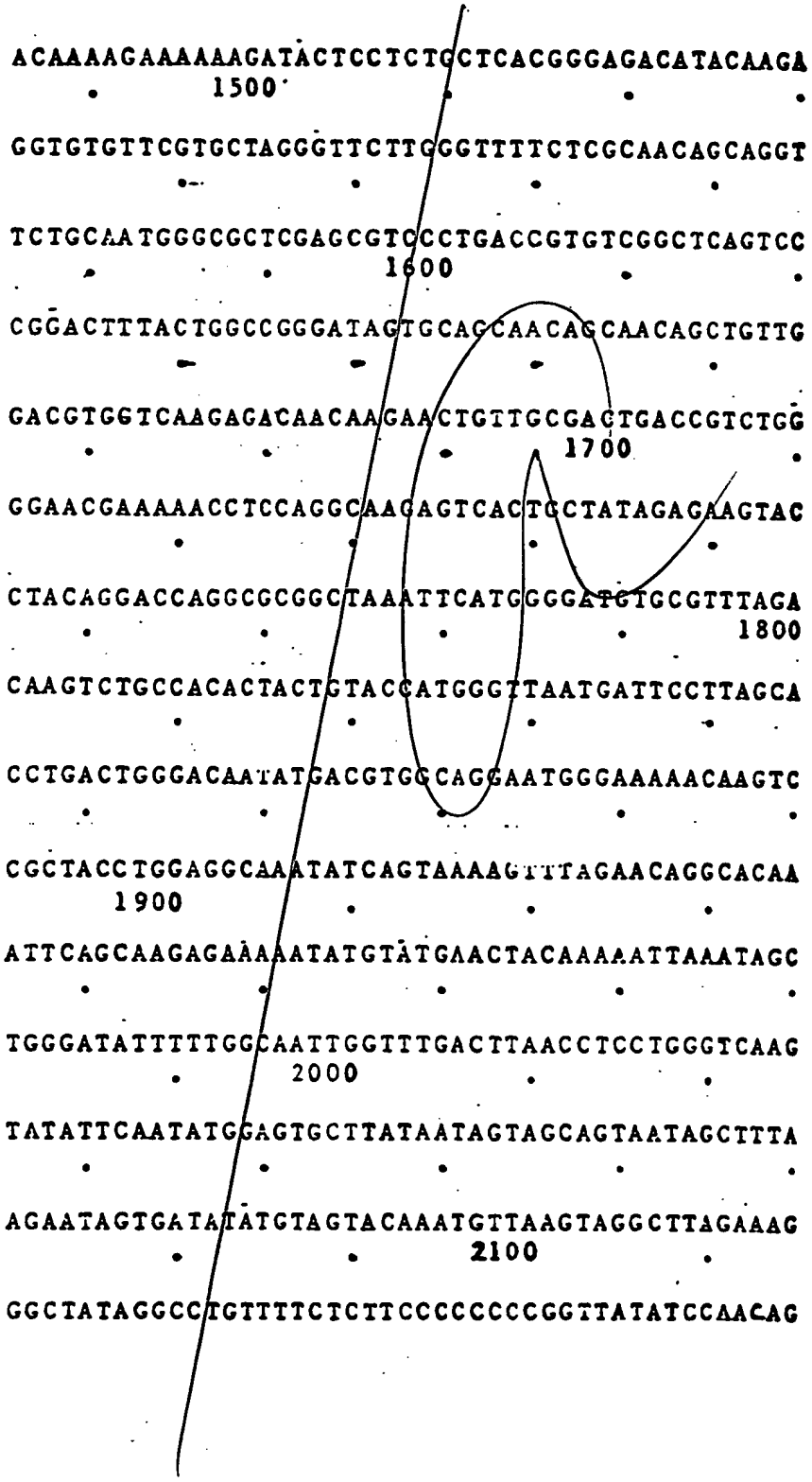
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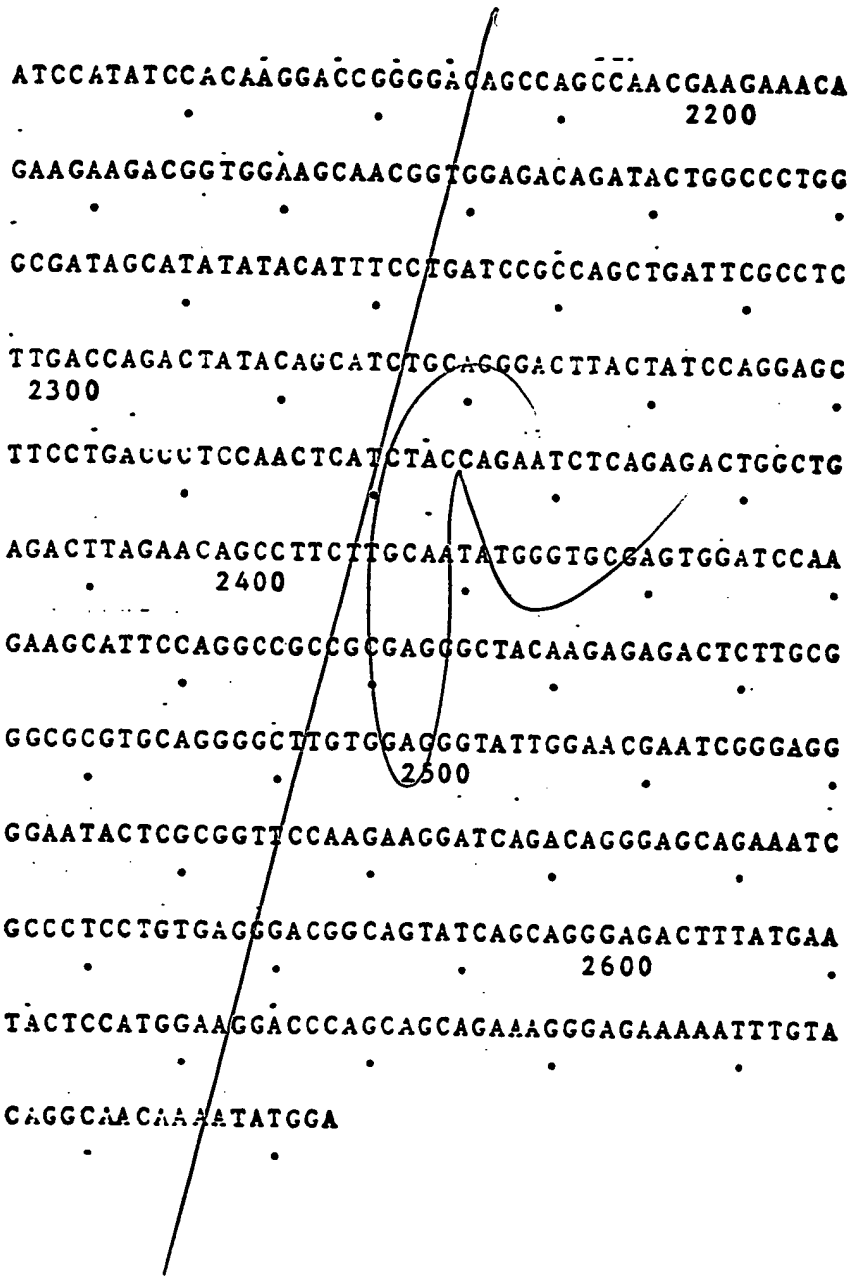
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2600
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7. The retrovirus of anyone of claims 1 to 6 whose RNA virtually hybridizes neither with the ENV gene and the LTR close to it, particularly with the nucleotide sequence 5290-9130 of HIV-1, nor with the sequences of the POL region of the HIV-1 genome, particularly with the nucleotide sequence 2170-2240 of HIV-1.

8. A composition comprising at least one antigen, particularly a protein or glycoprotein of HIV-2 virus according to anyone of claims 1 to 7.

9. The composition of claim 8 which consists of total extract or lysate of said retrovirus.

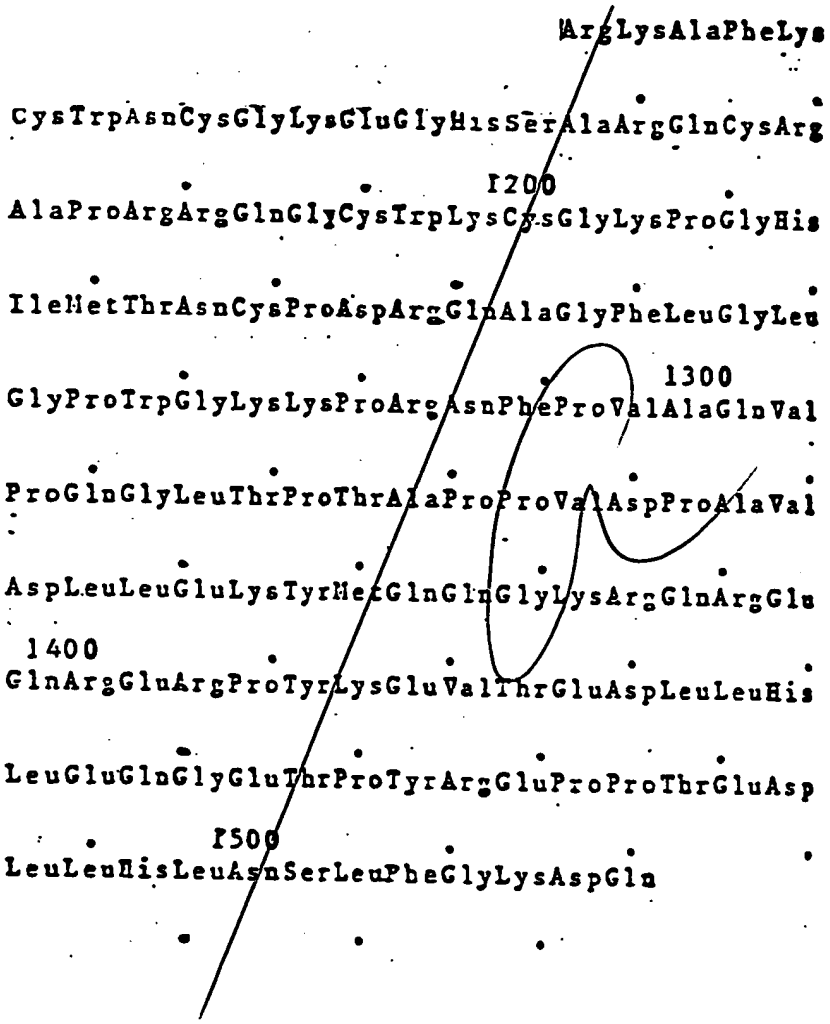
10. The composition of claim 8 wherein said antigen consists of at least one of the internal core proteins of said virus, particularly p12, p16 and p26, which have apparent molecular weight of the order of 12,000, 16,000 and 26,000.

11. The composition of claim 8, characterized in that it contains a gp140 glycoprotein having an apparent molecular weight of about 130,000-140,000.

12. An antigen which provides a single bound in electrophoresis on a polyacrylamid gel which comprises, in common with one of the purified antigens of HIV-2 retrovirus, an epitope that is recognized by the serum of a carrier of antibody against HIV-2.

13. A purified antigen having the immunological characteristics of one of the following proteins or glycoproteins of HIV-2: p12, p16, p26, p36, p42 and gp140.

14. An antigen of claim 13 which has the following aminoacid sequence or a part of said sequence recognized by anti-p12 antibodies :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1400
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LeuGluGlnGlyGluThrProTyrArgGluProProThrGluAsp
1500
LeuLeuHisLeuAsnSerLeuPheGlyLysAspGln

15. An antigen of claim 13 which has the following aminoacid sequence or a part of said sequence recognized by anti-p16 antibodies :

MetGlyAlaArgAsnSerValLeuArgGlyLysLysAlaAspGlu

LeuGluArgIleArgLeuArgProGlyGlyLysLysLysTyrArg

LeuLysHisIleValTrpAlaAlaAsnLysLeuAspArgPheGly

100

LeuAlaGluSerLeuLeuGluSerLysGluGlyCysGlnLysIle

LeuThrValLeuAspProMetValProThrGlySerGluAsnLeu

200

LysSerLeuPheAsnThrValCysValIleTrpCysIleHisAla

GluGluLysValLysAspThrGluGlyAlaLysGlnIleValArg

300

ArgHisLeuValAlaGluThrGlyThrAlaGluLysMetProSer

ThrSerArgProThrAlaProSerSerGluLysGlyGlyAsnTyr

400

46

16. An antigen of claim 13 which has the following aminoacid sequence or a part of said sequence recognized by anti-p26 antibodies :

ProValGlnHisValGlyGlyAsnTyrThrHisIleProLeuSer

ProArgThrLeuAsnAlaTrpValLysLeuValGluGluLysLys

PheGlyAlaGluValValProGlyPheGlnAlaLeuSerGluGly

500

CysThrProTyrAspIleAsnGlnMetLeuAsnCysValGlyAsp

HisGlnAlaAlaMetGlnIleIleArgGluIleIleAsnGluGlu

600

AlaAlaGluTrpAspValGlnHisProIleProGlyProLeuPro

AlaGlyGlnLeuArgGluProArgGlySerAspIleAlaGlyThr

700

ThrSerThrValGluGluGlnIleGlnTrpMetPheArgProGln

AsnProValProValGlyAsnIleTyrArgArgTrpIleGlnIle

800

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AspIleLysGlnGlyProLysGluProPheGlnSerTyrValAsp

900

ArgPheTyrLysSerLeuArgAlaGluGlnThrAspProAlaVal

LysAsnTrpMetThrGlnThrLeuLeuValGlnAsnAlaAsnPro

AspCysLysLeuValLeuLysGlyLeuGlyMetAsnProThrLeu

1000

GluGluMetLeuThrAlaCysGlnGlyValGlyGlyProGlyGln

LysAlaArgLeuMetAlaGluAlaLeuLysGluValIleGlyPro

1100

AlaProIleProPheAlaAlaAlaGlnGln

17. An antigen of claim 13 which has the following aminoacid sequence or a part of said sequence recognized by anti-gp140 antibodies :

ENVRN

MetMetAsnGlnLeuLeuIleAlaIleLeuLeuAlaSerAlaCys

LeuValTyrCysThrGlnTyrValThrValPheTyrGlyValPro

ThrTrpLysAsnAlaThrIleProLeuPheCysAlaThrArgAsn

100

ArgAspThrTrpGlyThrIleGlnCysLeuProAspAsnAspAsp

TyrGlnGluIleThrLeuAsnValThrGluAlaPheAspAlaTrp

200

AsnAsnThrValThrGluGlnAlaIleGluAspValTrpHisLeu

PheGluThrSerIleLysProCysValLysLeuThrProLeuCys

300

ValAlaMetLysCysSerSerThrGluSerSerThrGlyAsnAsn

ThrThrSerLysSerThrSerThrThrThrThrThrProThrAsp

400

GlnGluGlnGluIleSerGluAspThrProCysAlaArgAlaAsp

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500

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AsnGlnThrGlnCysTyrMetAsnHisCysAsnThrSerValIle

600

ThrGluSerCysAspLysHisTyrTrpAspAlaIleArgPheArg

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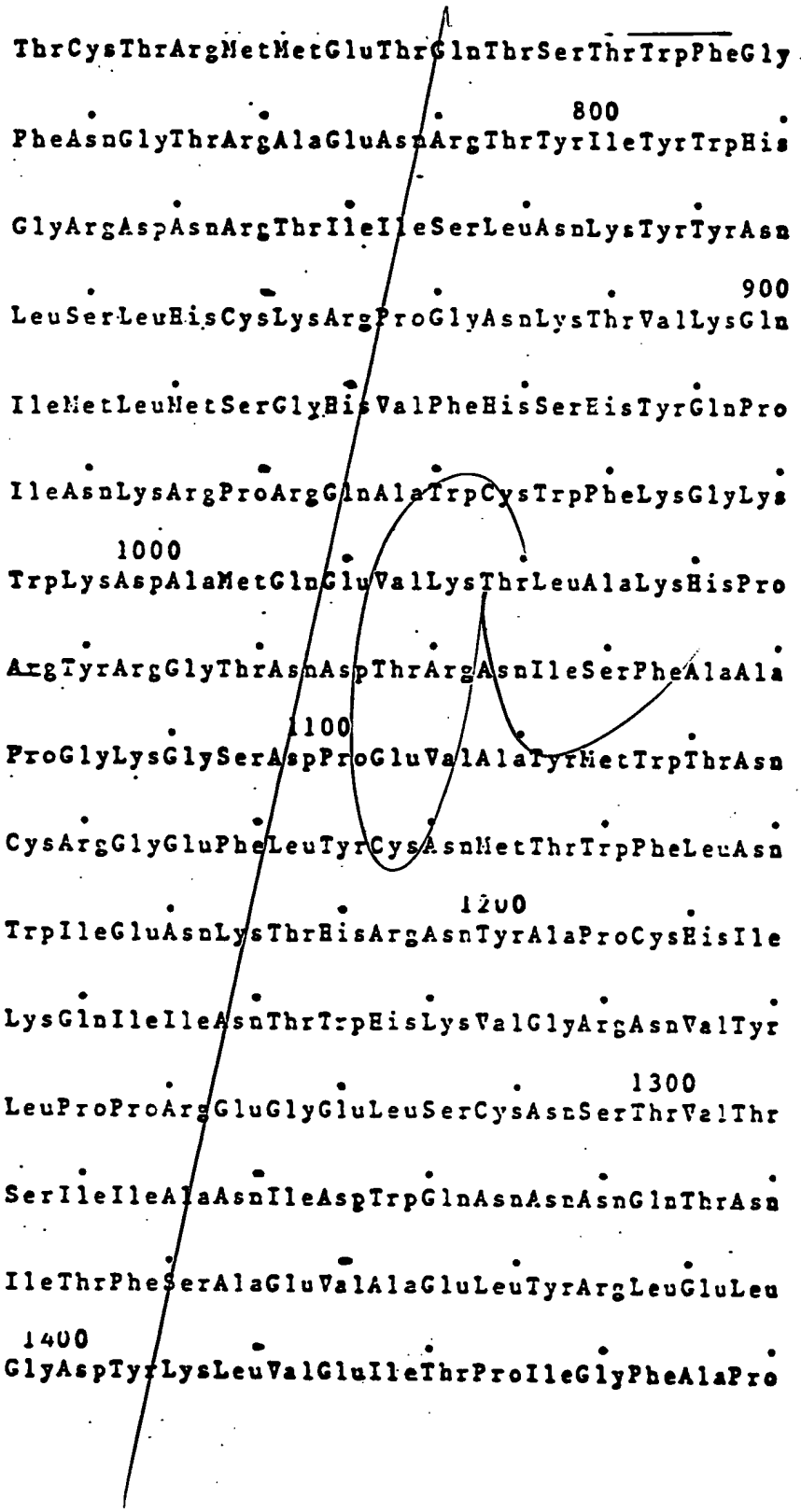
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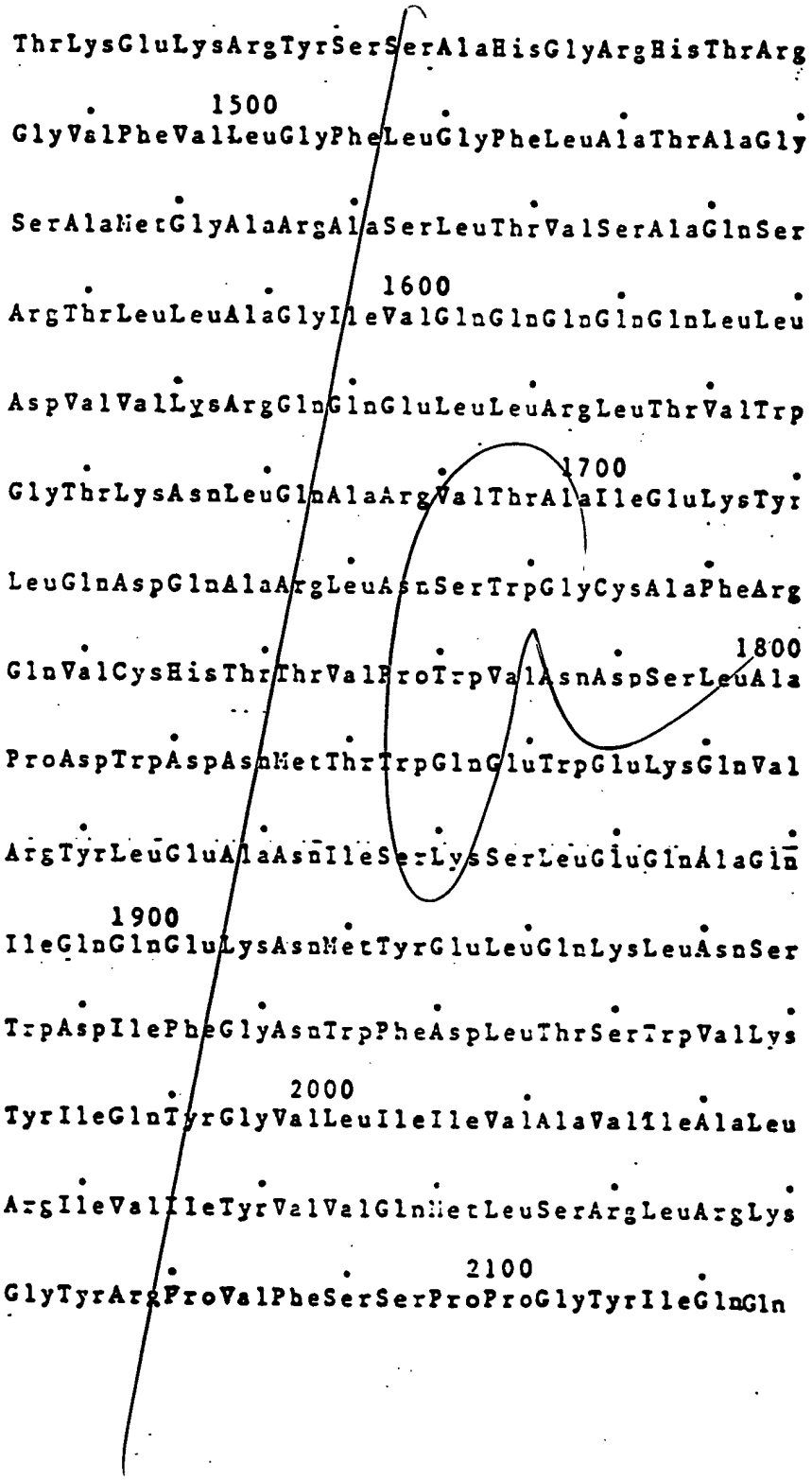
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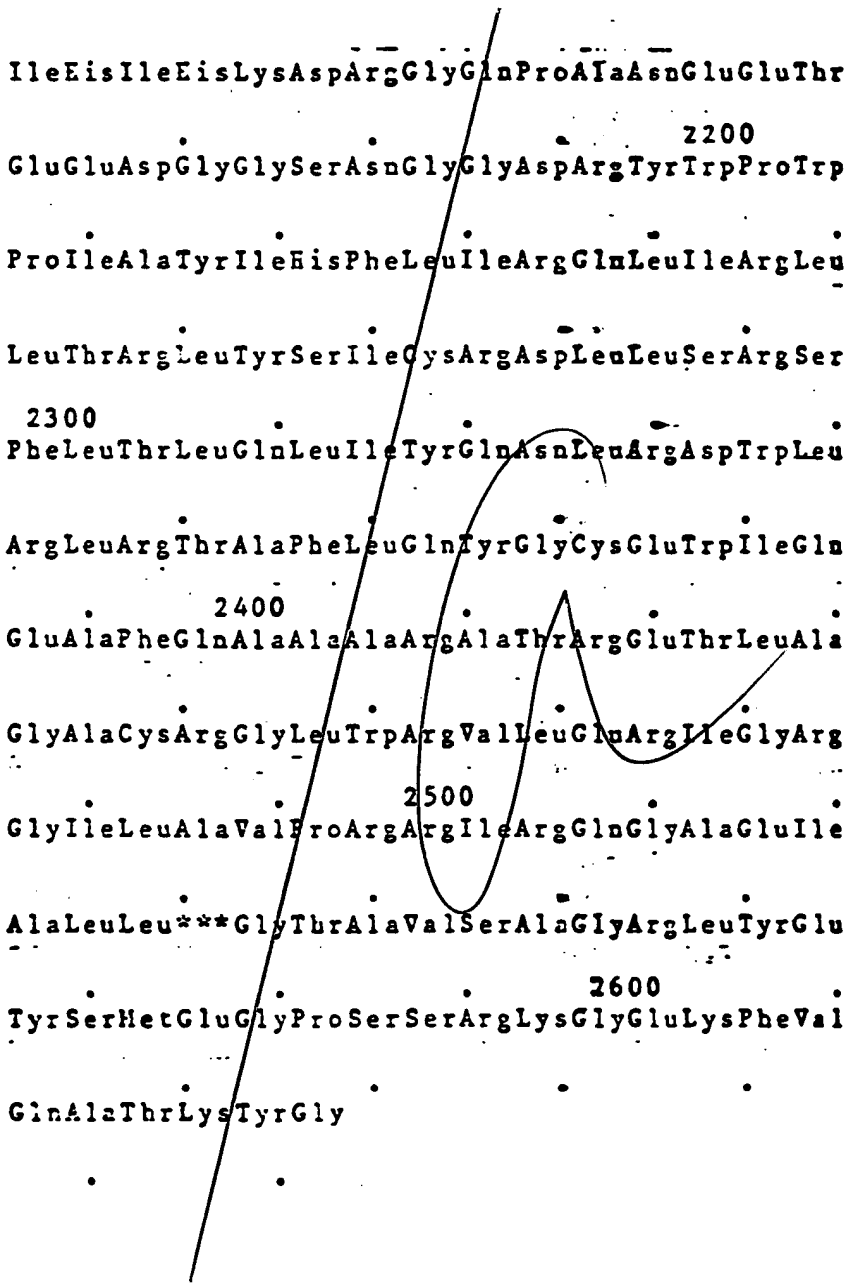
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2600
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18. A method for the in vitro detection of the presence of antibodies against anti-HIV-2 in a biological liquid, such as a serum, more particularly for the in vitro diagnosis of a potential or existing LAS or AIDS caused by HIV-2 type retrovirus, which comprises contacting a serum or other biological medium from the person to be diagnosed with a composition according to anyone of claims 8 to 11 or with an antigen according to anyone of claims 12 to 17, detecting the immunological conjuguate possibly formed between said anti-HIV-2-antibodies and the antigen or antigens used.

19. The method of claim 18 which comprises achieving the detection of said immunological conjuguate by reacting said immunological conjuguate possibly formed with a labelled reagent formed either by human anti-immunoglobulin-antibodies or of a bacterial A protein, and by detecting the complexe formed between the reagent and said immunological conjuguate.

20. Kit for the detection of anti-HIV-2-antibodies in a biological fluid, particularly of a person possibly carrying such antibodies, which comprises :

- a composition such as defined in anyone of claims 8 to 11 or an antigen such as defined in any of claims 12 to 17 ; and
- means for detecting the immunological complexe resulting from the immunological reaction between the antigen and said biological fluid.

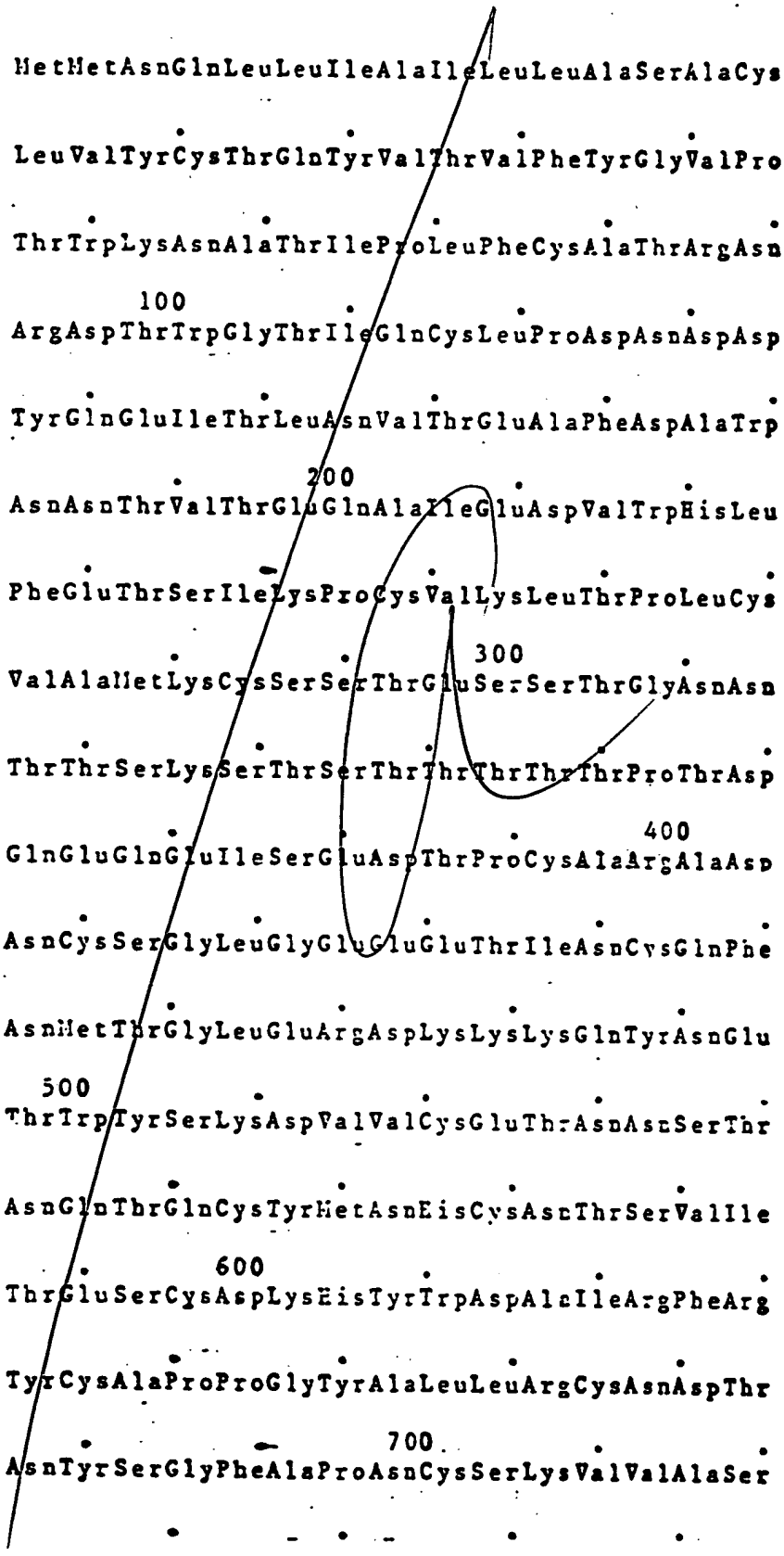
21. The kit of claim 21, whose means for detecting the immunological complexe formed comprises human anti-immunoglobulins or a protein A and a means for detecting the complexe formed between the anti-HIV-2 antibodies contained in the detected immunological conjuguate.

22. Immunogenic compositions containing an envelope glycoprotein of HIV-2 retrovirus, such as gp140

of said retrovirus, or part of said glycoprotein, in association with a pharmaceutically acceptable vehicle appropriate for the constitution of vaccines effective against HIV-2.

23. The composition of claim 22 which contains at least part of an immunogenic glycoprotein comprising the proteic backbone having the following sequence :

ENVRN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700
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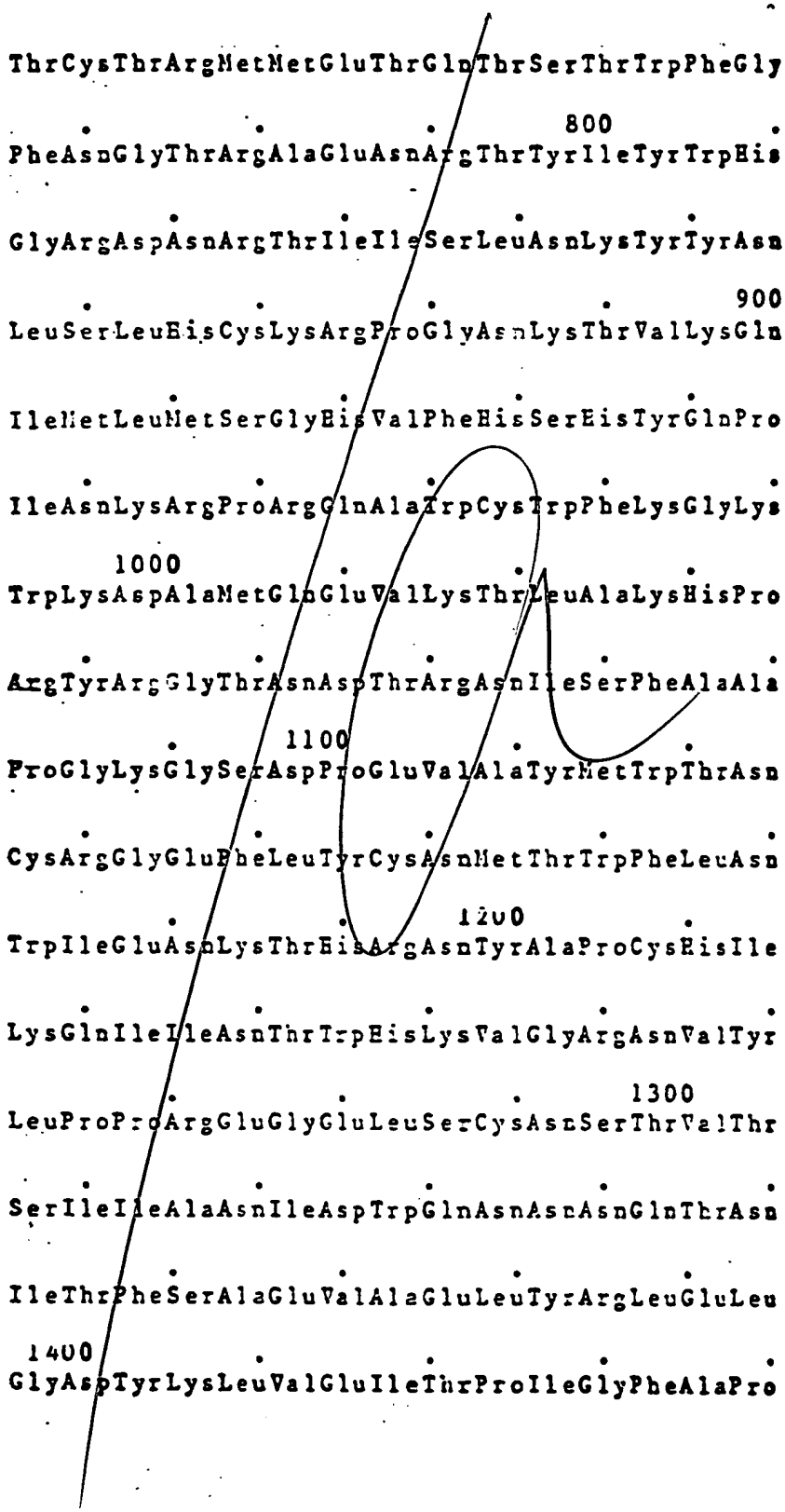
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GlyArgAspAsnArgThrIleIleSerLeuAsnLysTyrTyrAsn
900
LeuSerLeuHisCysLysArgProGlyAsnLysThrValLysGln
IleMetLeuMetSerGlyHisValPheHisSerHisTyrGlnPro
IleAsnLysArgProArgGlnAlaTrpCysTrpPheLysGlyLys
1000
TrpLysAspAlaMetGlnGluValLysThrLeuAlaLysHisPro
ArgTyrArgGlyThrAsnAspThrArgAsnIleSerPheAlaAla
1100
ProGlyLysGlySerAspProGluValAlaTyrMetTrpThrAsn
CysArgGlyGluPheLeuTyrCysAsnMetThrTrpPheLeuAsn
1200
TrpIleGluAsnLysThrHisArgAsnTyrAlaProCysHisIle
LysGlnIleIleAsnThrTrpHisLysValGlyArgAsnValTyr
1300
LeuProProArgGluGlyGluLeuSerCysAsnSerThrValThr
SerIleIleAlaAsnIleAspTrpGlnAsnAsnAsnGlnThrAsn
IleThrPheSerAlaGluValAlaGluLeuTyrArgLeuGluLeu
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1500
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1700
GlyThrLysAsnLeuGlnAlaArgValThrAlaIleGluLysTyr
LeuGlnAspGlnAlaArgLeuAsnSerTrpGlyCysAlaPheArg
1800
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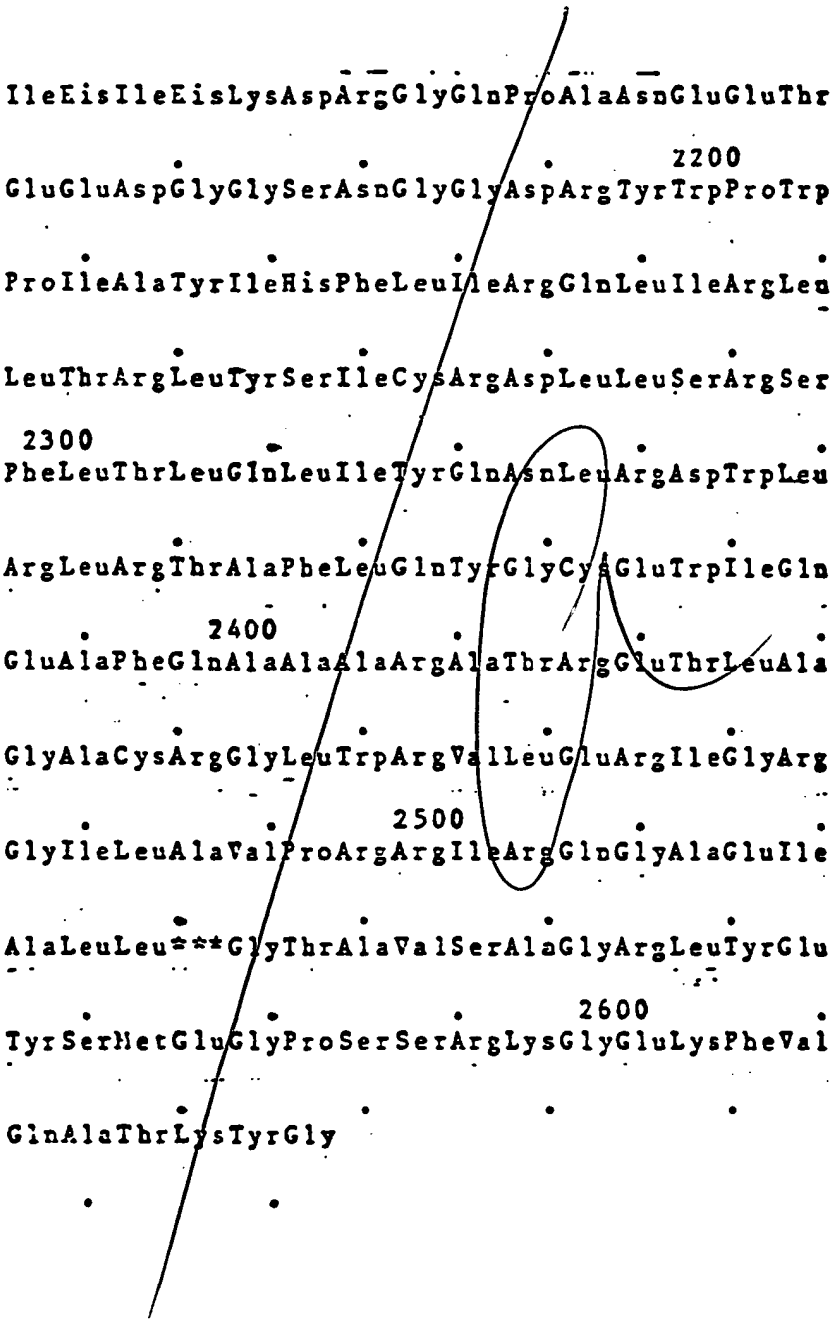
ProAspTrpAspAsnMetThrTrpGlnGluTrpGluLysGlnVal
ArgTyrLeuGluAlaAsnIleSerLysSerLeuGluGlnAlaGln
1900
IleGlnGlnGluLysAsnMetTyrGluLeuGlnLysLeuAsnSer
TrpAspIlePheGlyAsnTrpPheAspLeuThrSerTrpValLys
2000
TyrIleGlnTyrGlyValLeuIleIleValAlaValIleAlaLeu
ArgIleValIleTyrValValGlnMetLeuSerArgLeuArgLys
2100
GlyTyrArgProValPheSerSerProProGlyTyrIleGlnGln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ProIleAlaTyrIleHisPheLeuIleArgGlnLeuIleArgLeu
LeuThrArgLeuTyrSerIleCysArgAspLeuLeuSerArgSer
2300
PheLeuThrLeuGlnLeuIleTyrGlnAsnLeuArgAspTrpLeu
ArgLeuArgThrAlaPheLeuGlnTyrGlyCysGluTrpIleGln
2400
GluAlaPheGlnAlaAlaAlaArgAlaThrArgGluThrLeuAla
GlyAlaCysArgGlyLeuTrpArgValLeuGluArgIleGlyArg
2500
GlyIleLeuAlaValProArgArgIleArgGlnGlyAlaGluIle
AlaLeuLeu***GlyThrAlaValSerAlaGlyArgLeuTyrGlu
2600
TyrSerMetGluGlyProSerSerArgLysGlyGluLysPheVal
GlnAlaThrLysTyrGly

24. The immunogenic composition of claim 22 or of claim 23 which is dosed in antigen in order to enable the administration of a dosage-unit of 10 to 500, particularly from 50 to 100 µg/kg of bodyweight.

25. Monoclonal antibody characterized by its ability to specifically recognize one of the antigens according to anyone of claims 14 to 17.

26. The secreting hybridomas of the monoclonal antibody of claim 25.

27. Nucleic acids, optionally labelled, derived of part at least of RNA of HIV-2 virus or of one of its variance.

28. The nucleic acid of claim 27, which contains at least part of the cDNA which corresponds with the entire genomic RNA of HIV-2 retrovirus.

29. The nucleic acid of claim 27, which contains the nucleotide sequence :

GTGGAAGGCGAGACTGAAAGCAAGAGGAATACCATTTAGTTAAAGGACAG
GAACAGCTATACTTGGTCAGGGCAGGAAGTAACTAACAGAAACAGCTGAG
ACTGCAGGGACTTTCCAGAAGGGGCTGTAACCAAGGGAGGGACATGGGAG
GAGCTGGTGGGGAACGCCTCATATTCTCTGTATAATATACCCGCTGCTTG
CATTGTACTTCAGTCGCTCTGCGGAGAGGCTGGCAGATTGAGCCCTGGAG
GATCTCTCCAGCACTAGACGGATGAGCCTGGGTGCCCTGCTAGACTCTCA
CCAGCACTTGGCCGGTGCTGGCAGACGGCCCCACGCTTGCCTGCTTAAAA
ACCTTCCTTAATAAAGCTGCAGTAGAAGCA

30. The nucleic acid of claim 27, which contains a nucleotidic sequence coding for at least part of the aminoacid sequence indicated hereafter :

GAGRODN

MetGlyAlaArgAsnSerValLeuArgGlyLysLysAlaAspGlu

LeuGluArgIleArgLeuArgProGlyGlyLysLysLysTyrArg

LeuLysHisIleValTrpAlaAlaAsnLysLeuAspArgPheGly

100

LeuAlaGluSerLeuLeuGluSerLysGluGlyCysGlnLysIle

LeuThrValLeuAspProMetValProThrGlySerGluAsnLeu

200

LysSerLeuPheAsnThrValCysValIleTrpCysIleHisAla

GluGluLysValLysAspThrGluGlyAlaLysGlnIleValArg

300

ArgHisLeuValAlaGluThrGlyThrAlaGluLysMetProSer

ThrSerArgProThrAlaProSerSerGluLysGlyGlyAsnTyr

400

ProValGlnHisValGlyGlyAsnTyrThrHisIleProLeuSer

ProArgThrLeuAsnAlaTrpValLysLeuValGluGluLysLys

PheGlyAlaGluValValProGlyPheGlnAlaLeuSerGluGly

500

CysThrProTyrAspIleAsnGlnMetLeuAsnCysValGlyAsp

HisGlnAlaAlaMetGlnIleIleArgGluIleIleAsnGluGlu

600

AlaAlaGluTrpAspValGlnHisProIleProGlyProLeuPro

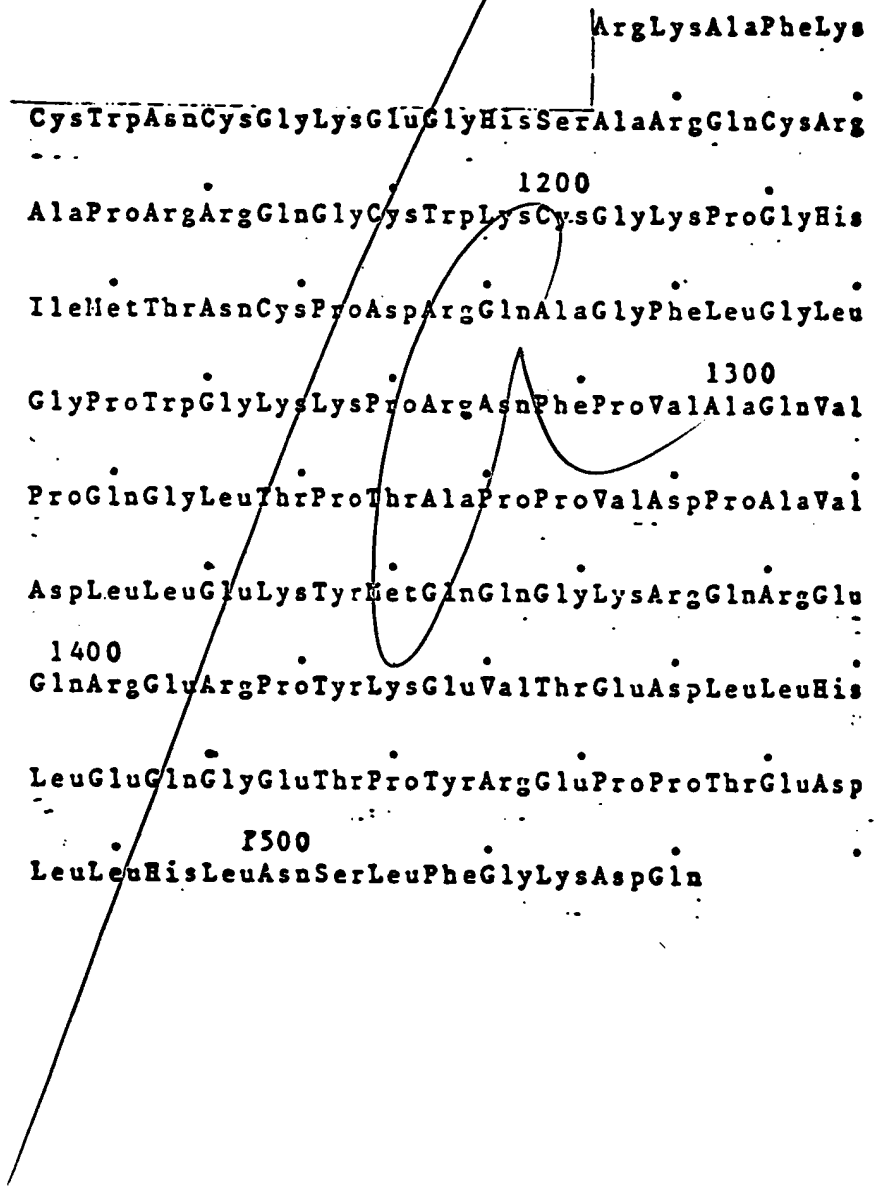
AlaGlyGlnLeuArgGluProArgGlySerAspIleAlaGlyThr

700

ThrSerThrValGluGluGlnIleGlnTrpMetPheArgProGln


AsnProValProValGlyAsnIleTyrArgArgTrpIleGlnIle
800
GlyLeuGlnLysCysValArgMetTyrAsnProThrAsnIleLeu
AspIleLysGlnGlyProLysGluProPheGlnSerTyrValAsp
900
ArgPheTyrLysSerLeuArgAlaGluGlnThrAspProAlaVal
LysAsnTrpMetThrGlnThrLeuLeuValGlnAsnAlaAsnPro
AspCysLysLeuValLeuLysGlyLeuGlyMetAsnProThrLeu
1000
GluGluMetLeuThrAlaCysGlnGlyValGlyGlyProGlyGln
LysAlaArgLeuMetAlaGluAlaLeuLysGluValIleGlyPro
1100
AlaProIleProPheAlaAlaAlaGlnGlnArgLysAlaPheLys
CysTrpAsnCysGlyLysGluGlyHisSerAlaArgGlnCysArg
1200
AlaProArgArgGlnGlyCysTrpLysCysGlyLysProGlyHis
IleMetThrAsnCysProAspArgGlnAlaGlyPheLeuGlyLeu
1300
GlyProTrpGlyLysLysProArgAsnPheProValAlaGlnVal
ProGlnGlyLeuThrProThrAlaProProValAspProAlaVal
AspLeuLeuGluLysTyrMetGlnGlnGlyLysArgGlnArgGlu
1400
GlnArgGluArgProTyrLysGluValThrGluAspLeuLeuHis
LeuGluGlnGlyGluThrProTyrArgGluProProThrGluAsp
1500
LeuLeuHisLeuAsnSerLeuPheGlyLysAspGln

31. The nucleic acid of claim 27, which contains a nucleotidic sequence coding for at least part of the aminoacid sequence indicated hereafter :



32. The nucleic acid of claim 27, which contains a nucleotidic sequence coding for at least part of the aminoacid sequence indicated hereafter :

MetGlyAlaArgAsnSerValLeuArgGlyLysLysAlaAspGlu

LeuGluArgIleArgLeuArgProGlyGlyLysLysLysTyrArg

LeuLysHisIleValTrpAlaAlaAsnLysLeuAspArgPheGly

100

LeuAlaGluSerLeuLeuGluSerLysGluGlyCysGlnLysIle

LeuThrValLeuAspProMetValProThrGlySerGluAsnLeu

200

LysSerLeuPheAsnThrValCysValIleTrpCysIleHisAla

GluGluLysValLysAspThrGluGlyAlaLysGlnIleValArg

300

ArgHisLeuValAlaGluThrGlyThrAlaGluLysMetProSer

ThrSerArgProThrAlaProSerSerGluLysGlyGlyAsnTyr

400

33. The nucleic acid of claim 27, which contains a nucleotidic sequence coding for at least part of the aminoacid sequence indicated hereafter :

ProValGlnHisValGlyGlyAsnTyrThrHisIleProLeuSer

ProArgThrLeuAsnAlaTrpValLysLeuValGluGluLysLys

PheGlyAlaGluValValProGlyPheGlnAlaLeuSerGluGly

500

CysThrProTyrAspIleAsnGlnMetLeuAsnCysValGlyAsp

HisGlnAlaAlaMetGlnIleIleArgGluIleIleAsnGluGlu

600

AlaAlaGluTrpAspValGlnHisProIleProGlyProLeuPro

AlaGlyGlnLeuArgGluProArgGlySerAspIleAlaGlyThr

700

ThrSerThrValGluGluGlnIleGlnTrpMetPheArgProGln

AsnProValProValGlyAsnIleTyrArgArgTrpIleGlnIle

800

GlyLeuGlnLysCysValArgMetTyrAsnProThrAsnIleLeu

AspIleLysGlnGlyProLysGluProPheGlnSerTyrValAsp

900

ArgPheTyrLysSerLeuArgAlaGluGlnThrAspProAlaVal

LysAsnTrpMetThrGlnThrLeuLeuValGlnAsnAlaAsnPro

AspCysLysLeuValLeuLysGlyLeuGlyMetAsnProThrLeu

1000

GluGluMetLeuThrAlaCysGlnGlyValGlyGlyProGlyGln

LysAlaArgLeuMetAlaGluAlaLeuLysGluValIleGlyPro

1100

AlaProIleProPheAlaAlaAlaGlnGln

34. The nucleic acid of claim 27, which contains a nucleotidic sequence coding for at least part of the aminoacid sequence indicated hereafter :

ENVRH

MetMetAsnGlnLeuLeuIleAlaIleLeuLeuAlaSerAlaCys

LeuValTyrCysThrGlnTyrValThrValPheTyrGlyValPro

ThrTrpLysAsnAlaThrIleProLeuPheCysAlaThrArgAsn

100

ArgAspThrTrpGlyThrIleGlnCysLeuProAspAsnAspAsp

TyrGlnGluIleThrLeuAsnValThrGluAlaPheAspAlaTrp

200

AsnAsnThrValThrGluGlnAlaIleGluAspValTrpHisLeu

PheGluThrSerIleLysProCysValLysLeuThrProLeuCys

300

ValAlaMetLysCysSerSerThrGluSerSerThrGlyAsnAsn

ThrThrSerLysSerThrSerThrThrThrThrThrProThrAsp

400

GlnGluGlnGluIleSerGluAspThrProCysAlaArgAlaAsp

AsnCysSerGlyLeuGlyGluGluGluThrIleAsnCysGlnPhe

AsnMetThrGlyLeuGluArgAspLysLysLysGlnTyrAsnGlu

500

ThrTrpTyrSerLysAspValValCysGluThrAsnAsnSerThr

AsnGlnThrGlnCysTyrMetAsnHisCysAsnThrSerValIle

600

ThrGluSerCysAspLysHisTyrTrpAspAlaIleArgPheArg

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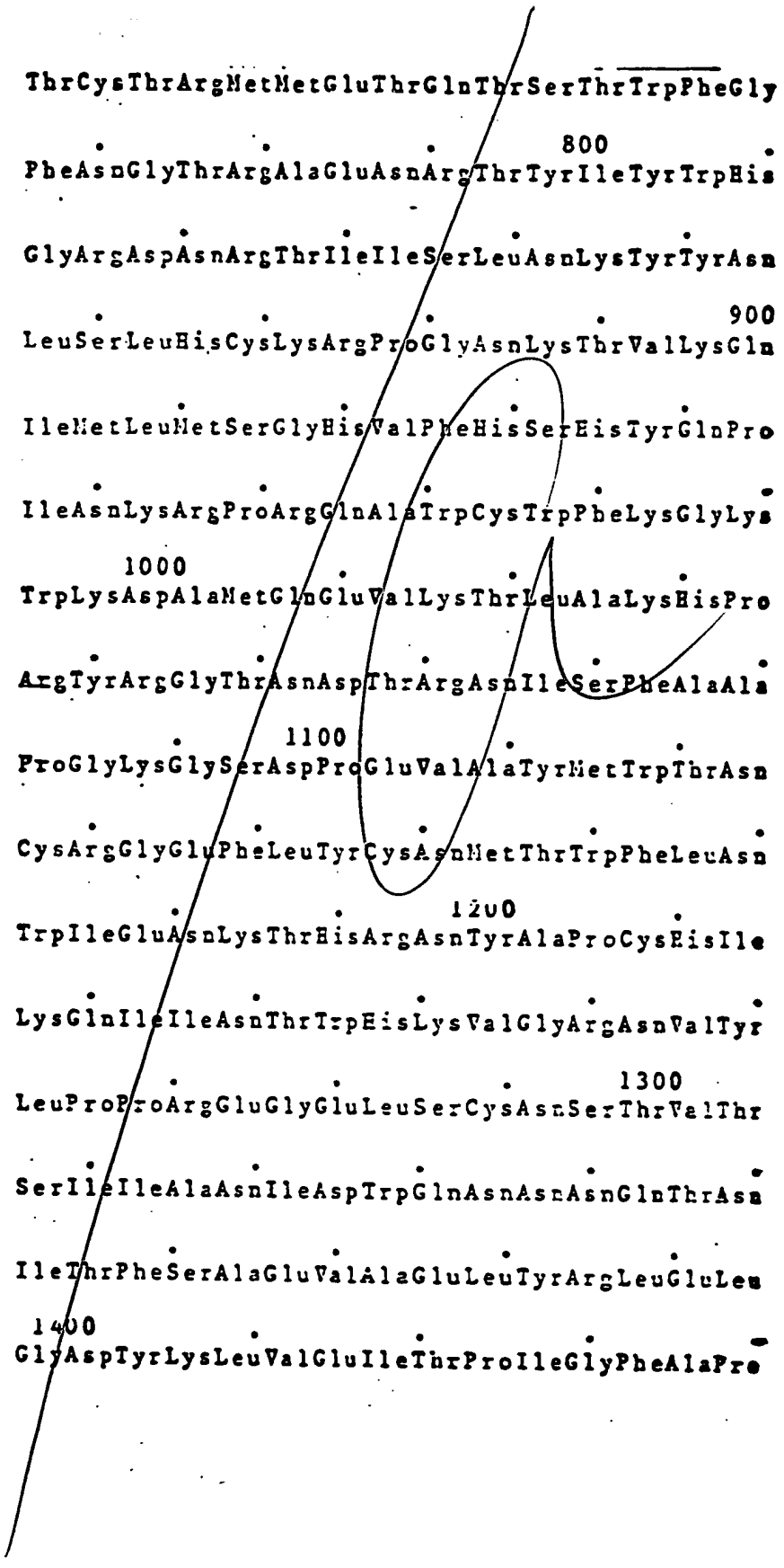
700

AsnTyrSerGlyPheAlaProAsnCysSerLysValValAlaSer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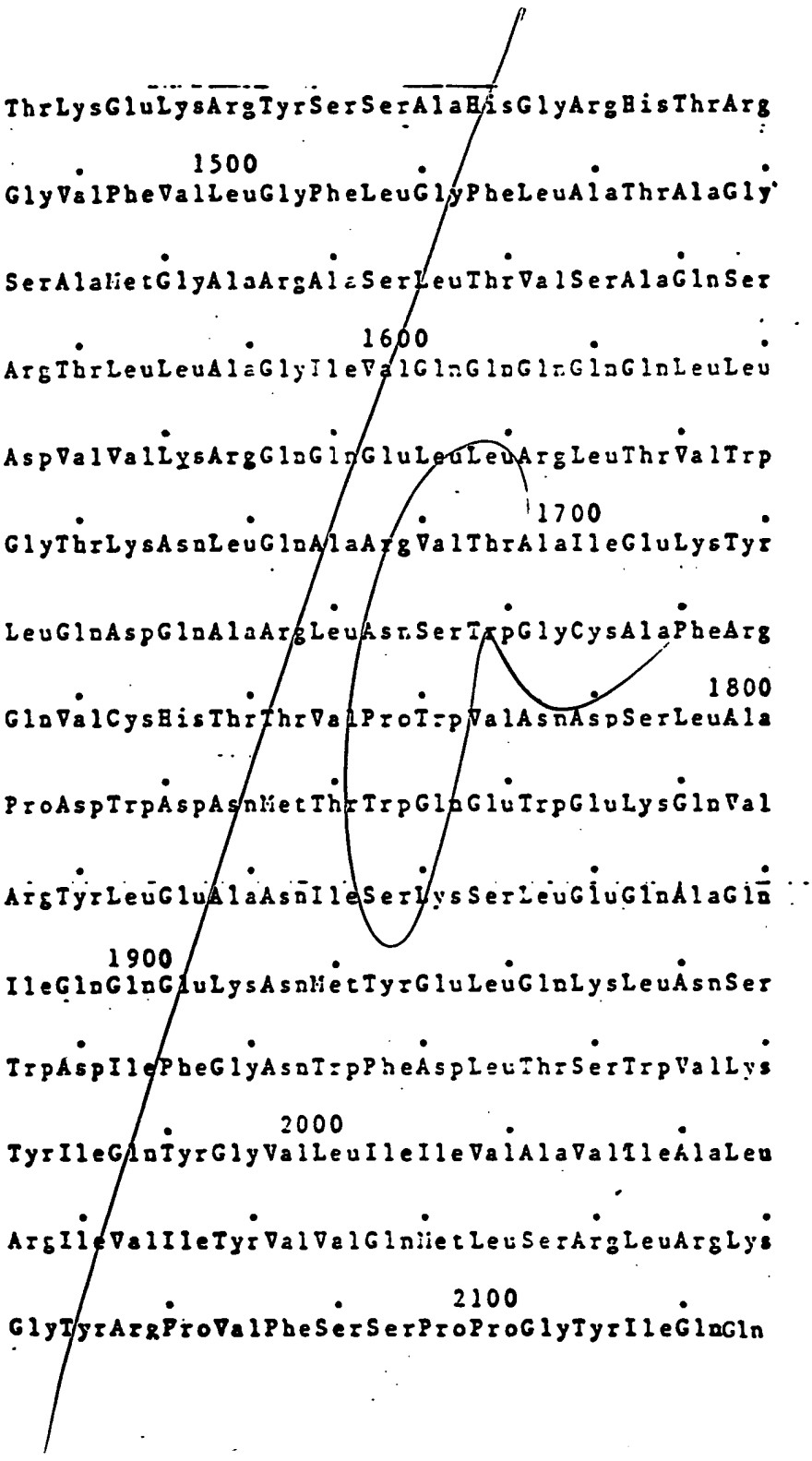
GlyArgAspAsnArgThrIleIleSerLeuAsnLysTyrTyrAsn
900
LeuSerLeuHisCysLysArgProGlyAsnLysThrValLysGln
IleMetLeuMetSerGlyHisValPheHisSerHisTyrGlnPro
IleAsnLysArgProArgGlnAlaTrpCysTrpPheLysGlyLys
1000
TrpLysAspAlaMetGlnGluValLysThrLeuAlaLysHisPro
ArgTyrArgGlyThrAsnAspThrArgAsnIleSerPheAlaAla
1100
ProGlyLysGlySerAspProGluValAlaTyrMetTrpThrAsn
CysArgGlyGluPheLeuTyrCysAsnMetThrTrpPheLeuAsn
1200
TrpIleGluAsnLysThrHisArgAsnTyrAlaProCysHisIle
LysGlnIleIleAsnThrTrpHisLysValGlyArgAsnValTyr
1300
LeuProProArgGluGlyGluLeuSerCysAsnSerThrValThr
SerIleIleAlaAsnIleAspTrpGlnAsnAsnAsnGlnThrAsn
IleThrPheSerAlaGluValAlaGluLeuTyrArgLeuGluLeu
1400
GlyAspTyrLysLeuValGluIleThrProIleGlyPheAlaPro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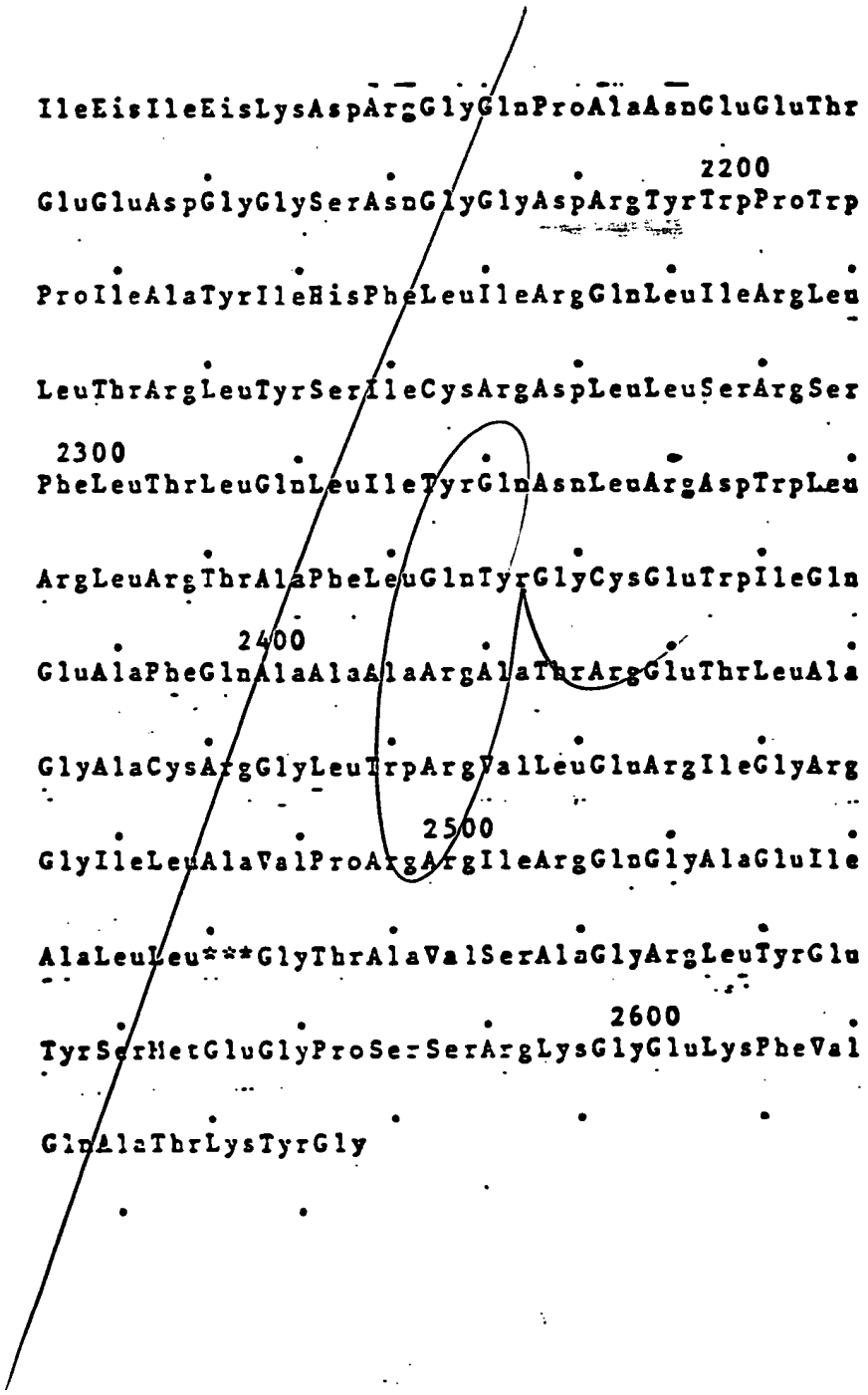
GlyValPheValLeuGlyPheLeuGlyPheLeuAlaThrAlaGly
SerAlaMetGlyAlaArgAlaSerLeuThrValSerAlaGlnSer
1600
ArgThrLeuLeuAlaGlyIleValGlnGlnGlnGlnGlnLeuLeu
AspValValLysArgGlnGlnGluLeuLeuArgLeuThrValTrp
1700
GlyThrLysAsnLeuGlnAlaArgValThrAlaIleGluLysTyr
LeuGlnAspGlnAlaArgLeuAsnSerTrpGlyCysAlaPheArg
1800
GlnValCysHisThrThrValProTrpValAsnAspSerLeuAla
ProAspTrpAspAsnMetThrTrpGlnGluTrpGluLysGlnVal
ArgTyrLeuGluAlaAsnIleSerLysSerLeuGluGlnAlaGln
1900
IleGlnGlnGluLysAsnMetTyrGluLeuGlnLysLeuAsnSer
TrpAspIlePheGlyAsnTrpPheAspLeuThrSerTrpValLys
2000
TyrIleGlnTyrGlyValLeuIleIleValAlaValIleAlaLeu
ArgIleValIleTyrValValGlnMetLeuSerArgLeuArgLys
2100
GlyTyrArgProValPheSerSerProProGlyTyrIleGlnGln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2300
PheLeuThrLeuGlnLeuIleTyrGlnAsnLeuArgAspTrpLeu
ArgLeuArgThrAlaPheLeuGlnTyrGlyCysGluTrpIleGln
2400
GluAlaPheGlnAlaAlaAlaArgAlaThrArgGluThrLeuAla
GlyAlaCysArgGlyLeuTrpArgValLeuGluArgIleGlyArg
2500
GlyIleLeuAlaValProArgArgIleArgGlnGlyAlaGluIle
AlaLeuLeu***GlyThrAlaValSerAlaGlyArgLeuTyrGlu
2600
TyrSerMetGluGlyProSerSerArgLysGlyGluLysPheVal
GlnAlaThrLysTyrGly

35. The nucleic acid of anyone of claims 28 to 34 which is formed a recombinant nucleic acid comprising a nucleic acid from a vector and in which said cDNA or part of said cDNA is inserted.

36. The recombinant nucleic acid of claim 35 which is labelled.

37. A process for the detection of HIV-2 retrovirus or of its RNA in a biological liquid or tissue, particularly for the in vitro diagnosis in man of the potentiality or existence of LAS or of AIDS, which comprises contacting nucleic acids contained in said biological liquid or tissue with a probe containing a nucleic acid according to anyone of claims 28 to 36 under stringent hybridization conditions for the time necessary for said hybridization to occur, washing the hybride formed with a solution ensuring the preservation of said stringent conditions, and detecting the hybride formed.

38. A process for the production of HIV-2 retrovirus which comprises culturing human T4 lymphocytes or permanent cell lines derived from said T4 lymphocytes and carrying the T4 phenotype, which lymphocytes or cell lines had previously been infected with an isolate of HIV-2 virus and, particularly when the level of reverse transcriptase activity has reached a determined threshold, recovering and purifying the amounts of virus released in the culture medium of said lymphocytes or cell lines, particularly by differential centrifugation in a gradient of sucrose or metrizamide.

39. A process for the production of specific antigen of HIV-2 retrovirus which comprises lysing, particularly by means of detergent such as SDS (for instance 0.1 % SDS in a RIPA buffer) and recovering the lysate containing said antigens;

40. Process for the production of one of the

above defined proteins (p12, p16 or p26) or of a protein having the structure of gp140 or of determined parts of said proteins, which process comprises inserting the corresponding nucleic acid sequence in a vector capable of transforming an appropriate host, enabling the expression of an insert containing in said vector, transforming said host by said vector which comprises the said nucleotidic sequence, culturing the transformed cell lines host, recovering and purifying the expressed protein.

41. Process for the production of a hybridization probe for the detection of the RNA of HIV-2 retrovirus which comprises a DNA sequence, particularly according to anyone of claims 27 to 35, in a cloning vector by <u>in vitro</u> recombination, cloning the modified vector obtained in a competent cellular host, and recovering the DNA-recombinants obtained.